

BE #7



PCT09

## RAW SEQUENCE LISTING

DATE: 05/15/2002

PATENT APPLICATION: US/09/980,526

TIME: 13:56:43

Input Set : A:\07039-278001.txt

Output Set: N:\CRF3\05152002\I980526.raw

ENTERED

4 <110> APPLICANT: Federspiel, Mark J.  
 6 <120> TITLE OF INVENTION: Methods to inhibit infectious agent transmission  
 8 <130> FILE REFERENCE: 07039-278001  
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/980,526  
 C--> 10 <141> CURRENT FILING DATE: 2001-11-15  
 10 <150> PRIOR APPLICATION NUMBER: US 09/980,526  
 11 <151> PRIOR FILING DATE: 2001-11-15  
 13 <150> PRIOR APPLICATION NUMBER: US 60/135,631  
 14 <151> PRIOR FILING DATE: 1999-05-24  
 16 <160> NUMBER OF SEQ ID NOS: 34  
 18 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
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 21 <211> LENGTH: 47  
 22 <212> TYPE: DNA  
 23 <213> ORGANISM: Artificial Sequence  
 25 <220> FEATURE:  
 26 <223> OTHER INFORMATION: Primer  
 28 <400> SEQUENCE: 1  
 29 gcgcattgcag atctgatgct taaacaggta gaaattttca ccgatgg 47  
 31 <210> SEQ ID NO: 2  
 32 <211> LENGTH: 45  
 33 <212> TYPE: DNA  
 34 <213> ORGANISM: Artificial Sequence  
 36 <220> FEATURE:  
 37 <223> OTHER INFORMATION: Primer  
 39 <400> SEQUENCE: 2  
 40 gctgctgcgt cgacttaaac ttcaacttgg tagcctgtat cttcc 45  
 42 <210> SEQ ID NO: 3  
 43 <211> LENGTH: 659  
 44 <212> TYPE: PRT  
 45 <213> ORGANISM: Porcine endogenous retrovirus  
 47 <400> SEQUENCE: 3  
 48 Met His Pro Thr Leu Ser Arg Arg His Leu Pro Ile Arg Gly Gly Lys  
 49 1 5 10 15  
 50 Pro Lys Arg Leu Lys Ile Pro Leu Ser Phe Ala Ser Ile Ala Trp Phe  
 51 20 25 30  
 52 Leu Thr Leu Ser Ile Thr Pro Gln Val Asn Gly Lys Arg Leu Val Asp  
 53 35 40 45  
 54 Ser Pro Asn Ser His Lys Pro Leu Ser Leu Thr Trp Leu Leu Thr Asp  
 55 50 55 60  
 56 Ser Gly Thr Gly Ile Asn Ile Asn Ser Thr Gln Gly Glu Ala Pro Leu  
 57 65 70 75 80  
 58 Gly Thr Trp Trp Pro Glu Leu Tyr Val Cys Leu Arg Ser Val Ile Pro

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59          85          90          95
60 Gly Leu Asn Asp Gln Ala Thr Pro Pro Asp Val Leu Arg Ala Tyr Gly
61          100          105          110
62 Phe Tyr Val Cys Pro Gly Pro Pro Asn Asn Glu Glu Tyr Cys Gly Asn
63          115          120          125
64 Pro Gln Asp Phe Phe Cys Lys Gln Trp Ser Cys Val Thr Ser Asn Asp
65          130          135          140
66 Gly Asn Trp Lys Trp Pro Val Ser Gln Gln Asp Arg Val Ser Tyr Ser
67 145          150          155          160
68 Phe Val Asn Asn Pro Thr Ser Tyr Asn Gln Phe Asn Tyr Gly His Gly
69          165          170          175
70 Arg Trp Lys Asp Trp Gln Gln Arg Val Gln Lys Asp Val Arg Asn Lys
71          180          185          190
72 Gln Ile Ser Cys His Ser Leu Asp Leu Asp Tyr Leu Lys Ile Ser Phe
73          195          200          205
74 Thr Glu Lys Gly Lys Gln Glu Asn Ile Gln Lys Trp Val Asn Gly Met
75          210          215          220
76 Ser Trp Gly Ile Val Tyr Tyr Arg Gly Ser Gly Arg Lys Lys Gly Ser
77 225          230          235          240
78 Val Leu Thr Ile Arg Leu Arg Ile Glu Thr Gln Met Glu Pro Pro Val
79          245          250          255
80 Ala Ile Gly Pro Asn Lys Gly Leu Ala Glu Gln Gly Pro Pro Ile Gln
81          260          265          270
82 Glu Gln Arg Pro Ser Pro Asn Pro Ser Asp Tyr Asn Thr Thr Ser Gly
83          275          280          285
84 Ser Val Pro Thr Glu Pro Asn Ile Thr Ile Lys Thr Gly Ala Lys Leu
85          290          295          300
86 Phe Asn Leu Ile Gln Gly Ala Phe Gln Ala Leu Asn Ser Thr Thr Pro
87 305          310          315          320
88 Glu Ala Thr Ser Ser Cys Trp Leu Cys Leu Ala Ser Gly Pro Pro Tyr
89          325          330          335
90 Tyr Glu Gly Met Ala Arg Gly Gly Lys Phe Asn Val Thr Lys Glu His
91          340          345          350
92 Arg Asp Gln Cys Thr Trp Gly Ser Gln Asn Lys Leu Thr Leu Thr Glu
93          355          360          365
94 Val Ser Gly Lys Gly Thr Cys Ile Gly Met Val Pro Pro Ser His Gln
95          370          375          380
96 His Leu Cys Asn His Thr Glu Ala Phe Asn Arg Thr Ser Glu Ser Gln
97 385          390          395          400
98 Tyr Leu Val Pro Gly Tyr Asp Arg Trp Trp Ala Cys Asn Thr Gly Leu
99          405          410          415
100 Thr Pro Cys Val Ser Thr Leu Val Phe Asn Gln Thr Lys Asp Phe Cys
101          420          425          430
102 Val Met Val Gln Ile Val Pro Arg Val Tyr Tyr Tyr Pro Glu Lys Ala
103          435          440          445
104 Val Leu Asp Glu Tyr Asp Tyr Arg Tyr Asn Arg Pro Lys Arg Glu Pro
105          450          455          460
106 Ile Ser Leu Thr Leu Ala Val Met Leu Gly Leu Gly Val Ala Ala Gly
107 465          470          475          480

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```

108 Val Gly Thr Gly Thr Ala Ala Leu Ile Thr Gly Pro Gln Gln Leu Glu
109                               485                               490                               495
110 Lys Gly Leu Ser Asn Leu His Arg Ile Val Thr Glu Asn Leu Gln Ala
111                               500                               505                               510
112 Leu Glu Lys Ser Val Ser Asn Leu Glu Glu Ser Leu Thr Ser Leu Ser
113                               515                               520                               525
114 Glu Val Val Leu Gln Asn Arg Arg Gly Leu Asp Leu Leu Phe Leu Lys
115                               530                               535                               540
116 Glu Gly Gly Leu Cys Val Ala Leu Lys Glu Glu Cys Cys Phe Tyr Val
117 545                               550                               555                               560
118 Asp His Ser Gly Ala Ile Arg Asp Ser Met Asn Lys Leu Arg Glu Arg
119                               565                               570                               575
120 Leu Glu Lys Arg Arg Arg Glu Lys Glu Thr Thr Gln Gly Trp Phe Glu
121                               580                               585                               590
122 Gly Trp Phe Asn Arg Ser Pro Trp Leu Ala Thr Leu Leu Ser Ala Leu
123                               595                               600                               605
124 Thr Gly Pro Leu Ile Val Leu Leu Leu Leu Leu Thr Val Gly Pro Cys
125 610                               615                               620
126 Ile Ile Asn Lys Leu Ile Ala Phe Ile Arg Glu Arg Ile Ser Ala Val
127 625                               630                               635                               640
128 Gln Ile Met Val Leu Arg Gln Gln Tyr Gln Ser Pro Ser Ser Arg Glu
129                               645                               650                               655
130 Ala Gly Arg
133 <210> SEQ ID NO: 4
134 <211> LENGTH: 660
135 <212> TYPE: PRT
136 <213> ORGANISM: Porcine endogenous retrovirus
138 <400> SEQUENCE: 4
139 Met His Pro Thr Leu Ser Arg Arg His Leu Pro Ile Arg Gly Gly Lys
140 1                               5                               10                               15
141 Pro Lys Arg Leu Lys Ile Pro Leu Ser Phe Ala Ser Ile Ala Trp Phe
142 20                               25                               30
143 Leu Thr Leu Ser Ile Thr Pro Gln Val Asn Gly Lys Arg Leu Val Asp
144 35                               40                               45
145 Ser Pro Asn Ser His Lys Pro Leu Ser Leu Thr Trp Leu Leu Thr Asp
146 50                               55                               60
147 Ser Gly Thr Gly Ile Asn Ile Asn Ser Thr Gln Gly Glu Ala Pro Leu
148 65                               70                               75                               80
149 Gly Thr Trp Trp Pro Glu Leu Tyr Val Cys Leu Arg Ser Val Ile Pro
150 85                               90                               95
151 Gly Leu Asn Asp Gln Ala Thr Pro Pro Asp Val Leu Arg Ala Tyr Gly
152 100                              105                              110
153 Phe Tyr Val Cys Pro Gly Pro Pro Asn Asn Glu Glu Tyr Cys Gly Asn
154 115                              120                              125
155 Pro Gln Asp Phe Phe Cys Lys Gln Trp Ser Cys Ile Thr Ser Asn Asp
156 130                              135                              140
157 Gly Asn Trp Lys Trp Pro Val Ser Gln Gln Asp Arg Val Ser Tyr Ser
158 145                              150                              155                               160
159 Phe Val Asn Asn Pro Thr Ser Tyr Asn Gln Phe Asn Tyr Gly His Gly

```

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```

160                               165                               170                               175
161 Arg Trp Lys Asp Trp Gln Gln Arg Val Gln Lys Asp Val Arg Asn Lys
162                               180                               185                               190
163 Gln Ile Ser Cys His Ser Leu Asp Leu Asp Tyr Leu Lys Ile Ser Phe
164                               195                               200                               205
165 Thr Glu Lys Gly Lys Gln Glu Asn Ile Gln Lys Trp Val Asn Gly Ile
166                               210                               215                               220
167 Ser Trp Gly Ile Val Tyr Tyr Gly Gly Ser Gly Arg Lys Lys Gly Ser
168 225                               230                               235                               240
169 Val Leu Thr Ile Arg Leu Arg Ile Glu Thr Gln Met Glu Pro Pro Val
170                               245                               250                               255
171 Ala Ile Gly Pro Asn Lys Gly Leu Ala Glu Gln Gly Pro Pro Ile Gln
172                               260                               265                               270
173 Glu Gln Arg Pro Ser Pro Asn Pro Ser Asp Tyr Asn Thr Thr Ser Gly
174                               275                               280                               285
175 Ser Val Pro Thr Glu Pro Asn Ile Thr Ile Lys Thr Gly Ala Lys Leu
176                               290                               295                               300
177 Phe Ser Leu Ile Gln Gly Ala Phe Gln Ala Leu Asn Ser Thr Thr Pro
178 305                               310                               315                               320
179 Glu Ala Thr Ser Ser Cys Trp Leu Cys Leu Ala Ser Gly Pro Pro Tyr
180                               325                               330                               335
181 Tyr Glu Gly Met Ala Arg Gly Gly Lys Phe Asn Val Thr Lys Glu His
182                               340                               345                               350
183 Arg Asp Gln Cys Thr Trp Gly Ser Gln Asn Lys Leu Thr Leu Thr Glu
184                               355                               360                               365
185 Val Ser Gly Lys Gly Thr Cys Ile Gly Met Val Pro Pro Ser His Gln
186                               370                               375                               380
187 His Leu Cys Asn His Thr Glu Ala Phe Asn Arg Thr Ser Glu Ser Gln
188 385                               390                               395                               400
189 Tyr Leu Val Pro Gly Tyr Asp Arg Trp Trp Ala Cys Asn Thr Gly Leu
190                               405                               410                               415
191 Thr Pro Cys Val Ser Thr Leu Val Phe Asn Gln Thr Lys Asp Phe Cys
192                               420                               425                               430
193 Val Met Val Gln Ile Val Pro Arg Val Tyr Tyr Tyr Pro Glu Lys Ala
194                               435                               440                               445
195 Val Leu Asp Glu Tyr Asp Tyr Arg Tyr Asn Arg Pro Lys Arg Glu Pro
196                               450                               455                               460
197 Ile Ser Leu Thr Leu Ala Val Met Leu Gly Leu Gly Val Ala Ala Gly
198 465                               470                               475                               480
199 Val Gly Thr Gly Thr Ala Ala Leu Ile Thr Gly Pro Gln Gln Leu Glu
200                               485                               490                               495
201 Lys Gly Leu Ser Asn Leu His Arg Ile Val Thr Glu Asp Leu Gln Ala
202                               500                               505                               510
203 Leu Glu Lys Ser Val Ser Asn Leu Glu Glu Ser Leu Thr Ser Leu Ser
204                               515                               520                               525
205 Glu Val Val Leu Gln Asn Arg Arg Gly Leu Asp Leu Leu Phe Leu Lys
206                               530                               535                               540
207 Glu Gly Gly Leu Cys Val Ala Leu Lys Glu Glu Cys Cys Phe Tyr Val
208 545                               550                               555                               560

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```

209 Asp His Ser Gly Ala Ile Arg Asp Ser Met Ser Lys Leu Arg Glu Arg
210          565          570          575
211 Leu Glu Arg Arg Arg Arg Glu Arg Glu Ala Asp Gln Gly Trp Phe Glu
212          580          585          590
213 Gly Trp Phe Asn Arg Ser Pro Trp Met Thr Thr Leu Leu Ser Ala Leu
214          595          600          605
215 Thr Gly Pro Leu Val Val Leu Leu Leu Leu Leu Thr Val Gly Pro Cys
216          610          615          620
217 Leu Ile Asn Arg Phe Val Ala Phe Val Arg Glu Arg Val Ser Ala Val
218 625          630          635          640
219 Gln Ile Met Val Leu Arg Gln Gln Tyr Gln Gly Leu Leu Ser Gln Gly
220          645          650          655
221 Glu Thr Asp Leu
222          660
224 <210> SEQ ID NO: 5
225 <211> LENGTH: 638
226 <212> TYPE: PRT
227 <213> ORGANISM: Porcine endogenous retrovirus
229 <400> SEQUENCE: 5
230 Met His Pro Thr Leu Asn Arg Arg His Leu Pro Ile Arg Gly Gly Lys
231 1          5          10          15
232 Pro Lys Arg Leu Lys Ile Pro Leu Ser Phe Ala Ser Ile Ala Trp Phe
233          20          25          30
234 Leu Thr Leu Ser Ile Thr Ser Gln Thr Asn Gly Met Arg Ile Gly Asp
235          35          40          45
236 Ser Leu Asn Ser His Lys Pro Leu Ser Leu Thr Trp Leu Ile Thr Asp
237          50          55          60
238 Ser Gly Thr Gly Ile Asn Ile Asn Asn Thr Gln Gly Glu Ala Pro Leu
239 65          70          75          80
240 Gly Thr Trp Trp Pro Asp Leu Tyr Val Cys Leu Arg Ser Val Ile Pro
241          85          90          95
242 Ser Leu Thr Ser Pro Pro Asp Ile Leu His Ala His Gly Phe Tyr Val
243          100         105         110
244 Cys Pro Gly Pro Pro Asn Asn Gly Lys His Cys Gly Asn Pro Arg Asp
245          115         120         125
246 Phe Phe Cys Lys Gln Trp Asn Cys Val Thr Ser Asn Asp Gly Tyr Trp
247          130         135         140
248 Lys Trp Pro Thr Ser Gln Gln Asp Arg Val Ser Phe Ser Tyr Val Asn
249 145          150         155         160
250 Thr Tyr Thr Ser Ser Gly Gln Phe Asn Tyr Leu Thr Trp Ile Arg Thr
251          165         170         175
252 Gly Ser Pro Lys Cys Ser Pro Ser Asp Leu Asp Tyr Leu Lys Ile Ser
253          180         185         190
254 Phe Thr Glu Lys Gly Lys Gln Glu Asn Ile Leu Lys Trp Val Asn Gly
255          195         200         205
256 Met Ser Trp Gly Met Val Tyr Tyr Gly Gly Ser Gly Lys Gln Pro Gly
257          210         215         220
258 Ser Ile Leu Thr Ile Arg Leu Lys Ile Asn Gln Leu Glu Pro Pro Met
259 225          230         235         240

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## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/980,526

DATE: 05/15/2002

TIME: 13:56:45

Input Set : A:\07039-278001.txt

Output Set: N:\CRF3\05152002\I980526.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:1040 M:283 W: Missing Blank Line separator, &lt;400&gt; field identifier

L:1077 M:283 W: Missing Blank Line separator, &lt;400&gt; field identifier